

REMARKS

As a result of Applicants' election of Group II and the species of SEQ ID NO:15, claims 1-16, 20, 21, 23, 25, 54-56, 58, 60, 62, 75, 77, 79, 81, 89-100, 108-111, 121-124, 130-133, 136-139, 144, 151-154, 158-163 and 166-173 have been withdrawn. Claims 18, 28, 31 and 146 are rejected under 35 U.S.C. § 102(b) as being anticipated by the public use of oligo-dT and oligo-U. Claims 17, 18, 26-32 and 146 are rejected under 35 U.S.C. § 102(a) as being anticipated by the TOR2 sequence (Genbank AY274119, version AY2741191.1, GI29826276). Claims 101, 115, 117, 125, 135 and 165 are rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the enablement requirement. Claim 26 is rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the written description requirement. Claims 17, 27, 29, 30, 32, 101, 115, 135, 146 and 165 are herein amended. Claims 18, 26, 28, 31 and 117 are herein cancelled without prejudice. New claims 174-178 are herein added. No new matter has been introduced. Claims 17, 27, 29, 30, 32, 101, 115, 125, 135, 146, 165 and 174-178 are pending in the case.

Reconsideration of the present application in view of the foregoing amendments and the remarks below is respectfully requested.

Priority

The Office Action states that the full-length sequence of strain HKU-39 strain SARS virus was first disclosed in 60/464,886 and, therefore, "the effective date for this species appears to be 6/23/2006 [*sic*]." Applicants assume that the Examiner intended to state "4/23/03", instead of "6/23/06."

Applicants respectfully submit that the full-length sequence of hSARS virus having China Center for Type Culture Collection Deposit Accession No. CCTCC-V200303 was first disclosed in provisional application serial no. 60/464,886, which was

filed April 23, 2003. Further, Applicants hereby confirm that the nucleotide sequence of SEQ ID NO:15 of the present application is the same as the sequence shown in Fig. 10 of provisional application no. 60/464,886.

Claim Rejections under 35 U.S.C. § 102

(1) Claims 18, 28, 31 and 146 are rejected under 35 U.S.C. § 102(b) as being anticipated by the public use of oligo-dT and oligo-U.

Claims 18, 28 and 31 are herein cancelled without prejudice to accelerate the prosecution of the case. Applicants expressly reserve a right to pursue the cancelled claims in a continuation application.

Accordingly, the rejection of claims 18, 28 and 31 are now moot.

Claim 146 is herein amended to recite that the nucleic acid molecule comprises "a nucleotide sequence having at least 8,000 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:15, or a complement thereof."

Support for the amendments can be found, for example, at page 3, lines 22-30.

In general, oligo-dT and oligo-U refer to short sequences of "Ts" or "Us", typically 20 or less base pairs. Claim 146 as amended requires that the nucleic acid molecule comprises at least 8,000 nucleotides in length.

Thus, claim 146 as amended is not anticipated by the public use of oligo-dT and oligo-U.

Accordingly, Applicants respectfully request that the rejection of claim 146 under 35 U.S.C. § 102(b) as anticipated by the public use of oligo-dT and oligo-U be withdrawn.

(2) Claims 17, 18, 26-32 and 146 are rejected under 35 U.S.C. § 102(a) as being anticipated by the TOR2 sequence (Genbank AY274119, version AY274119.1, GI29826276).

Claims 18, 26, 28 and 31 are herein cancelled without prejudice. Claims 29 and 32 are herein amended so as not to depend from cancelled claim 26. Thus, the rejection of these claims is now moot.

Claim 17 is herein amended to recite that the hSARS virus is the one "having China Center for Type Culture Collection Deposit Accession No. CCTCC-V200303, or a complement thereof."

Accordingly, claim 17 as amended is not anticipated by the TOR2 sequence.

Furthermore, claim 146 is herein amended as discussed in the previous section. The maximum number of identical contiguous nucleotides between SEQ ID NO:15 and TOR2 is 7914. Claim 146 as amended requires that the nucleic acid molecule comprises at least 8,000 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:15, or a complement thereof and, therefore, is not anticipated by the TOR2 sequence.

Both claims 27 and 30 are herein amended to depend from claim 17 or 146 and, therefore, are not anticipated by the TOR2 sequence, either.

Accordingly, Applicants respectfully request that the rejection of claims 17, 27, 30 and 146 under 35 U.S.C. § 102(a) as being anticipated by the TOR2 sequence be withdrawn.

Claim Rejections under 35 U.S.C. § 112

(1) Claims 101, 115, 117, 125, 135 and 165 are rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the enablement requirement.

Specifically, the Office Action states that “[t]hese claims are drawn to pharmaceutical compositions comprising SEQ ID NO:15. The specification does not teach how to use the full-length genomic sequence (or its complement) in any body-treating method, and its use seems inadvisable because it encodes a lethal virus” and that “it is concluded that undue experimentation would be required to use the full-length SARS genomic sequence in body-treating compositions, as claimed.”

Claim 117 is here in cancelled and, therefore, the rejection of claim 117 is now moot.

Claims 101, 115 and 165 are herein amended to recite that the nucleic acid molecule comprises “a portion of SEQ ID NO:15 having at least 8,000 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:15, or a complement thereof”, excluding the complete sequence of SEQ ID NO:15.

Support for the amendments can be found, for example, at page 3, lines 22-30, and at page 9, lines 5-24.

Based on the studies on other coronaviruses well known at the time of the filing of the present application and SEQ ID NO:15 disclosed in the present specification, one skilled in the art would have been able to predict most of the proteins

encoded by the genome, without undue experimentation. For example, all coronaviruses encode several homologous proteins, such as ORF1a, ORF1ab, S, M, E and N proteins, which are essential proteins for viral replication. Furthermore, based on the studies on other well-characterized coronaviruses, one skilled in the art would also have been able to predict the functions of the proteins encoded by SEQ ID NO:15. For example, among others, S proteins are known to induce neutralization antibody for vaccine purposes, whereas proteins from ORF1a and ORF1ab are essential for viral RNA transcription and replication and are possible targets for antiviral. Thus, based on studies of known coronaviruses, one skilled in the art would have been able to predict the characteristics of the viral proteins encoded by SEQ ID NO:15 without undue experimentation and use such information for therapeutic and/or vaccine purposes.

Thus, Applicants believe claim 101 and its dependent claim 125, claim 115 and its dependent claim 135, and claim 165 all meet the enablement requirement and, therefore, the rejection of these claims under 35 U.S.C. § 112, first paragraph, as failing to comply with the enablement requirement should be withdrawn.

(2) Claim 26 is rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the written description requirement.

Claim 26 is herein cancelled as discussed above.

Accordingly, the rejection of claim 26 is now moot.

New Claims

New claim 174 depends from claim 146 and is directed to the entire sequence of SEQ ID NO:15.

Support for claims 175-177 can be found, for example, Section 6.3 of the present specification.

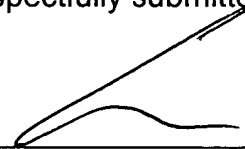
Support for claim 178 can be found, for example, Sections 5.2 and 5.6 of the present specification.

No new matter has been introduced by the new claims.

No fee, other than the extension fee, is believed to be due for this submission. Should there be any deficiency in fees, please charge such fee(s) to Deposit Account No. 50-2215.

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Respectfully submitted,

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